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REQUIREMENTS...SEQUENCE DISCLOSURES"**

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be submitted using one of the following methods:

1. Electronically submitted through EFS-Bio
(<http://www.uspto.gov/ebs/efs/downloads/documents.htm>, EFS Submission User Manual - ePAVE)
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RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/083,842
Source: OIPB
Date Processed by STIC: 3/19/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

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1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
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Revised 01/29/2002

Raw Sequence Listing Error Summary

01PE

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/083,842

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 ☒ Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☒ Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/083,842

DATE: 03/19/2002
TIME: 16:15:26

Input Set : A:\EP.txt
Output Set: N:\CRF3\03192002\J083842.raw

→ The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

3 <110> APPLICANT: Syngenta Biotechnology, Inc.
4 Grina, Jonas
6 <120> TITLE OF INVENTION: NOVEL CYANOENAMINES USEFUL AS LIGANDS FOR MODULATING GENE
EXPRESSION IN
7 PLANTS OR ANIMALS
9 <130> FILE REFERENCE: 1392/2/2
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/083,842
C--> 11 <141> CURRENT FILING DATE: 2002-02-27
11 <150> PRIOR APPLICATION NUMBER: 60/272,905
12 <151> PRIOR FILING DATE: 2001-03-02
14 <160> NUMBER OF SEQ ID NOS: 12
16 <170> SOFTWARE: PatentIn version 3.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 17
20 <212> TYPE: DNA
21 <213> ORGANISM: synthetic construct
23 <400> SEQUENCE: 1
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29 <212> TYPE: DNA
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37 <211> LENGTH: 36
38 <212> TYPE: DNA
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47 <212> TYPE: DNA
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64 aagtgcattg aacccttgct tcggatc 147

invalid response, see error summary sheet, item 10
4-11



RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/083,842

DATE: 03/19/2002

TIME: 16:15:26

Input Set : A:\EP.txt

Output Set: N:\CRF3\03192002\J083842.raw

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72 <220> FEATURE:
73 <221> NAME/KEY: CDS
74 <222> LOCATION: (361)..(2031)
75 <223> OTHER INFORMATION:
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83 cttcggattg tggtgtgact gaaaagcgac gcgtatcggt gtcgaagatt ctctataagt      180
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87 gttcatgccc gtagagacgc gtttagatag ttatggcgag gaaaaagtga agtgaaagcc      300
89 tacgtcagag gatgtccctc ggtggtcacg gaagccgggg cgtgtgacgc gctcttcgac      360
91 atg aga cgc cgc tgg tca aac aac gga tgt ttc cct ctg cga atg ttt      408
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96 Glu Glu Ser Ser Ser Glu Val Thr Ser Ser Ser Ala Phe Gly Met Pro
97          20          25          30
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100 Ala Ala Met Val Met Ser Pro Glu Ser Leu Ala Ser Pro Glu Tyr Gly
101          35          40          45
103 ggc ctc gag ctc tgg agc tac gat gag acc atg aca aac tat ccg gcg      552
104 Gly Leu Glu Leu Trp Ser Tyr Asp Glu Thr Met Thr Asn Tyr Pro Ala
105          50          55          60
107 cag tca ctg ctc ggc gcg tgt aat gcg ccg cag cag cag cag caa cag      600
108 Gln Ser Leu Leu Gly Ala Cys Asn Ala Pro Gln Gln Gln Gln Gln Gln
109 65          70          75          80
111 caa caa cag cag ccg tcc gct cag ccg ctg ccg tct atg ccg ctg ccg      648
112 Gln Gln Gln Gln Pro Ser Ala Gln Pro Leu Pro Ser Met Pro Leu Pro
113          85          90          95
115 atg cct cct aca act cct aaa tca gag aac gag tcc atg tcg tca ggt      696
116 Met Pro Pro Thr Thr Pro Lys Ser Glu Asn Glu Ser Met Ser Ser Gly
117          100          105          110
119 cga gaa gaa tta tca ccg gcc tca agt ata aat gga tgt agt act gat      744
120 Arg Glu Glu Leu Ser Pro Ala Ser Ser Ile Asn Gly Cys Ser Thr Asp
121          115          120          125
123 ggg gaa cca aga cga cag aag aaa ggg cca gcg ccg cgc cag cag gag      792
124 Gly Glu Pro Arg Arg Gln Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu
125          130          135          140
127 gaa ctg tgc ctt gtt tgc ggc gac agg gct tcg gga tat cac tat aac      840
128 Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn
129 145          150          155          160
131 gcg ctt acg tgc gaa gga tgt aaa ggg ttc ttc agg cgg agt gtg acc      888
132 Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr
133          165          170          175
135 aag aat gcg gta tat att tgt aaa ttt gga cac gcc tgc gag atg gac      936

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DATE: 03/19/2002

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Input Set : A:\EP.txt

Output Set: N:\CRF3\03192002\J083842.raw

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137				180					185					190			
139	atg	tac	atg	agg	aga	aaa	tgc	caa	gag	tgt	cgg	ttg	aag	aaa	tgc	ctc	984
140	Met	Tyr	Met	Arg	Arg	Lys	Cys	Gln	Glu	Cys	Arg	Leu	Lys	Lys	Cys	Leu	
141			195					200					205				
143	gcg	gtg	ggc	atg	agg	ccc	gag	tgc	gtc	gtc	cca	gag	tcc	acg	tgc	aag	1032
144	Ala	Val	Gly	Met	Arg	Pro	Glu	Cys	Val	Val	Pro	Glu	Ser	Thr	Cys	Lys	
145		210					215					220					
147	aac	aaa	aga	aga	gaa	aag	gaa	gca	cag	aga	gaa	aaa	gac	aaa	ctg	cca	1080
148	Asn	Lys	Arg	Arg	Glu	Lys	Glu	Ala	Gln	Arg	Glu	Lys	Asp	Lys	Leu	Pro	
149	225					230					235				240		
151	gtc	agt	acg	acg	aca	gtg	gac	gat	cat	atg	cct	gcc	ata	atg	caa	tgt	1128
152	Val	Ser	Thr	Thr	Thr	Val	Asp	Asp	His	Met	Pro	Ala	Ile	Met	Gln	Cys	
153				245						250					255		
155	gac	cct	ccg	ccc	cca	gag	gcg	gca	agg	att	cac	gaa	gtg	gtc	ccg	agg	1176
156	Asp	Pro	Pro	Pro	Pro	Glu	Ala	Ala	Arg	Ile	His	Glu	Val	Val	Pro	Arg	
157			260					265						270			
159	ttc	cta	acg	gag	aag	cta	atg	gag	cag	aac	aga	ctg	aag	aat	gtg	acg	1224
160	Phe	Leu	Thr	Glu	Lys	Leu	Met	Glu	Gln	Asn	Arg	Leu	Lys	Asn	Val	Thr	
161			275					280					285				
163	ccg	ctg	tcg	gcg	aac	cag	aag	tcc	ctg	atc	gcg	agg	ctc	gtg	tgg	tac	1272
164	Pro	Leu	Ser	Ala	Asn	Gln	Lys	Ser	Leu	Ile	Ala	Arg	Leu	Val	Trp	Tyr	
165		290					295					300					
167	cag	gag	ggg	tac	gag	cag	ccg	tcg	gag	gaa	gat	ctc	aag	aga	gtt	aca	1320
168	Gln	Glu	Gly	Tyr	Glu	Gln	Pro	Ser	Glu	Glu	Asp	Leu	Lys	Arg	Val	Thr	
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171	cag	aca	tgg	cag	tta	gaa	gaa	gaa	gaa	gag	gag	gaa	act	gac	atg	ccc	1368
172	Gln	Thr	Trp	Gln	Leu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Thr	Asp	Met	Pro	
173				325						330					335		
175	ttc	cgt	cag	atc	aca	gag	atg	acg	atc	tta	aca	gtg	cag	ctt	att	gta	1416
176	Phe	Arg	Gln	Ile	Thr	Glu	Met	Thr	Ile	Leu	Thr	Val	Gln	Leu	Ile	Val	
177			340					345						350			
179	gaa	ttc	gca	aag	gga	cta	ccg	gga	ttc	tcc	aag	ata	tct	cag	tcc	gat	1464
180	Glu	Phe	Ala	Lys	Gly	Leu	Pro	Gly	Phe	Ser	Lys	Ile	Ser	Gln	Ser	Asp	
181		355					360						365				
183	caa	att	aca	tta	tta	aag	gcg	tca	tca	agc	gaa	gtg	atg	atg	ctg	cga	1512
184	Gln	Ile	Thr	Leu	Leu	Lys	Ala	Ser	Ser	Ser	Glu	Val	Met	Met	Leu	Arg	
185		370					375					380					
187	gtg	gcg	cga	cgg	tac	gac	gcg	gcg	acg	gac	agc	gtg	ctg	ttc	gcg	aac	1560
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189	385					390					395				400		
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192	Asn	Gln	Ala	Tyr	Thr	Arg	Asp	Asn	Tyr	Arg	Lys	Ala	Gly	Met	Ser	Tyr	
193				405						410					415		
195	gtc	atc	gag	gac	ctg	ctg	cac	ttc	tgt	cgg	tgt	atg	tac	tcc	atg	agc	1656
196	Val	Ile	Glu	Asp	Leu	Leu	His	Phe	Cys	Arg	Cys	Met	Tyr	Ser	Met	Ser	
197			420					425					430				
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200	Met	Asp	Asn	Val	His	Tyr	Ala	Leu	Leu	Thr	Ala	Ile	Val	Ile	Phe	Ser	

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Output Set: N:\CRF3\03192002\J083842.raw

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205          450          455          460
207 tac tac ttg aag acg ctg cgg gtt tac att tta aat cag cac agc gcg      1800
208 Tyr Tyr Leu Lys Thr Leu Arg Val Tyr Ile Leu Asn Gln His Ser Ala
209 465          470          475          480
211 tcg cct cgc tgc gcc gtg ctg ttc ggc aag atc ctc ggc gtg ctg acg      1848
212 Ser Pro Arg Cys Ala Val Leu Phe Gly Lys Ile Leu Gly Val Leu Thr
213          485          490          495
215 gaa ctg cgc acg ctc ggc acg cag aac tcc aac atg tgc atc tcg ctg      1896
216 Glu Leu Arg Thr Leu Gly Thr Gln Asn Ser Asn Met Cys Ile Ser Leu
217          500          505          510
219 aag ctg aag aac agg aaa ctt ccg cca ttc ctc gag gag atc tgg gac      1944
220 Lys Leu Lys Asn Arg Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp Asp
221          515          520          525
223 gtg gcc gaa gtg tcg acg acg cag ccg acg ccg ggg gtg gcg gcg cag      1992
224 Val Ala Glu Val Ser Thr Thr Gln Pro Thr Pro Gly Val Ala Ala Gln
225          530          535          540
227 gtg acc ccc atc gtg gtg gac aac ccc gcg gcg ctc tag ctggcgcgcc      2041
228 Val Thr Pro Ile Val Val Asp Asn Pro Ala Ala Leu
229 545          550          555
231 ggcgcgcgcgc cccgcgcgcc ccgcgcgcgc cgctcccccg cgccgcgcgc gcgcgcgcgc 2101
233 gcggcctgcg ctgagtgcgg gacccgcgcc gagagagaaa cgctcataga ctggctagtt 2161
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239 gattagtgaat tatatgtgtt gttgaacgtt tggagagtat atttagtggt gatcgtcggg 2341
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276          35          40          45
279 Gly Leu Glu Leu Trp Ser Tyr Asp Glu Thr Met Thr Asn Tyr Pro Ala
280          50          55          60

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/083,842

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Input Set : A:\EP.txt

Output Set: N:\CRF3\03192002\J083842.raw

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284 65 70 75 80
287 Gln Gln Gln Gln Pro Ser Ala Gln Pro Leu Pro Ser Met Pro Leu Pro
288 85 90 95
291 Met Pro Pro Thr Thr Pro Lys Ser Glu Asn Glu Ser Met Ser Ser Gly
292 100 105 110
295 Arg Glu Glu Leu Ser Pro Ala Ser Ser Ile Asn Gly Cys Ser Thr Asp
296 115 120 125
299 Gly Glu Pro Arg Arg Gln Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu
300 130 135 140
303 Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn
304 145 150 155 160
307 Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr
308 165 170 175
311 Lys Asn Ala Val Tyr Ile Cys Lys Phe Gly His Ala Cys Glu Met Asp
312 180 185 190
315 Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu
316 195 200 205
319 Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Ser Thr Cys Lys
320 210 215 220
323 Asn Lys Arg Arg Glu Lys Glu Ala Gln Arg Glu Lys Asp Lys Leu Pro
324 225 230 235 240
327 Val Ser Thr Thr Thr Val Asp Asp His Met Pro Ala Ile Met Gln Cys
328 245 250 255
331 Asp Pro Pro Pro Pro Glu Ala Ala Arg Ile His Glu Val Val Pro Arg
332 260 265 270
335 Phe Leu Thr Glu Lys Leu Met Glu Gln Asn Arg Leu Lys Asn Val Thr
336 275 280 285
339 Pro Leu Ser Ala Asn Gln Lys Ser Leu Ile Ala Arg Leu Val Trp Tyr
340 290 295 300
343 Gln Glu Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Lys Arg Val Thr
344 305 310 315 320
347 Gln Thr Trp Gln Leu Glu Glu Glu Glu Glu Glu Thr Asp Met Pro
348 325 330 335
351 Phe Arg Gln Ile Thr Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val
352 340 345 350
355 Glu Phe Ala Lys Gly Leu Pro Gly Phe Ser Lys Ile Ser Gln Ser Asp
356 355 360 365
359 Gln Ile Thr Leu Leu Lys Ala Ser Ser Ser Glu Val Met Met Leu Arg
360 370 375 380
363 Val Ala Arg Arg Tyr Asp Ala Ala Thr Asp Ser Val Leu Phe Ala Asn
364 385 390 395 400
367 Asn Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ser Tyr
368 405 410 415
371 Val Ile Glu Asp Leu Leu His Phe Cys Arg Cys Met Tyr Ser Met Ser
372 420 425 430
375 Met Asp Asn Val His Tyr Ala Leu Thr Ala Ile Val Ile Phe Ser
376 435 440 445
379 Asp Arg Pro Gly Leu Glu Gln Pro Leu Leu Val Glu Glu Ile Gln Arg

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/083,842

DATE: 03/19/2002

TIME: 16:15:28

Input Set : A:\EP.txt

Output Set: N:\CRF3\03192002\J083842.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date